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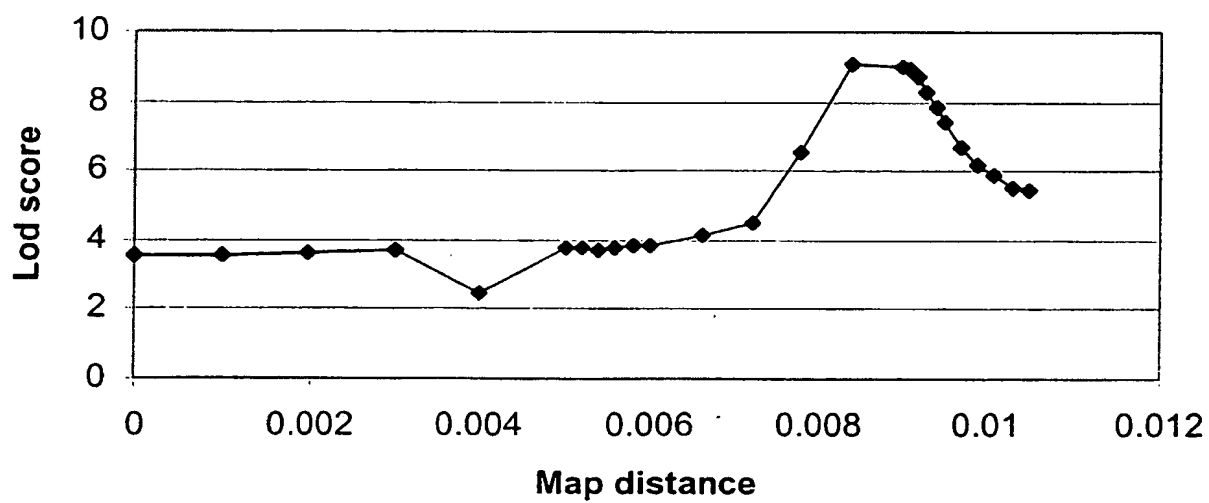


Figure 1



170 180
Pig TAC CGC ACC ATC CAA GAT TTG GGC ATC GGC ACA TTC CGA GAC TTG GCC GTG GTG CTG GAA
Tyr Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val Val Leu Glu
Hum --- --- --T --- --- --- --- --- --- --- --- --- --T --- --- --- --G
190 200
Pig ACG GCG CCC ATC CTG ACC GCA CTG GAC ATC TTC GTG GAC CGG CGT GTG TCT GCG CTG CCT
Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp Arg Arg Val Ser Ala Leu Pro
Hum --A --A --- --- --- --T --- --- --- --- --T --- --- --- --- --A --- ---
210 220
Pig GTG GTC AAC GAA ACT GGA CAG GTA GTG GGC CTC TAC TCT CGC TTT GAT GTG ATC CAC CTG
Val Val Asn Glu Thr Gly Gln Val Val Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu
Hum --- --- --- --- TG- --T --- --C --- --- --T --C --- --- --- --T --- ---
Cys - - - - -
230 240
Pig GCT GCC CAA CAA ACA TAC AAC CAC CTG GAC ATG AAT GTG GGA GAA GCC CTG AGG CAG CGG
Ala Ala Gln Gln Thr Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg
Hum --- --- --G --- --C --- --- --- --- --- --G- --- --- --- --- --- A--
Ser - - - - -
250 260
Pig ACA CTG TGT CTG GAA GGC GTC CTT TCC TGC CAG CCC CAC GAG ACC TTG GGG GAA GTC ATT
Thr Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly Glu Val Ile
Hum --- --A --- --- --G --A --- --- --- --- --- --G- --- --- --- --G --C
Ser - - - - -
270 280
Pig GAC CGG ATT GTC CGG GAA CAG GTG CAC CGC CTG GTG CTC GTG GAT GAG ACC CAG CAC CTT
Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu Val Asp Glu Thr Gln His Leu
Hum --- A-- --- -CT --- --G --- --A --- A-G --- --- --A --- --C --- --- --T --C
Ala - - - - -
290 300
Pig CTG GGC GTG GTG TCC CTC TCT GAC ATC CTT CAG GCT CTG GTG CTC AGC CCT GCT GGA ATT
Leu Gly Val Val Ser Leu Ser Asp Ile Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile
Hum T-- --- --- --C --- --- --C --- --- --- --A --- --- --- --- --C --C
CDS
Pig GAT GCC CTC GGG GCC TGA
Asp Ala Leu Gly Ala ***
Hum --- --- --- --- ---
3'UTR 10 20 30 40 50 60 70 80
Pig GAACCTTGGAACCTTTGCTCTCAGGCCACCTGGCACACCTGGAAGCCAGTGAAGGGAGCCGTGGACTCAGCTCTCACTTC
Hum ---GA-CT--GT-C-CAA--C--A---A-----A-----A-T....AGAA-----T---
90 100 110 120 130 140 150 160
Pig CCCTCAGCCCCACTTGGTCTGGTCTCTTGTTCAGGTAGGCTCCGCCCGGGGC....CCCTGGCCTCAGCATCAGCCC
Hum ---A.-C---A-T-----TCA---A-GA-----CTTCT--A---TTCCAAAATTG--T-T---T--T-GT--T-
170 180 190 200 210 220 230 240
Pig CTCAGTCTCCCT.GGGCACCCAGATCTCAGACTGGGGCACCCCTGAAGATG.GGAGTGGCCAGCTTATAGCTGAGCAG.C
Hum ----AAC--T-C-----TG-CC-GTG--CCA-----TGA---AT-AA---AACAG-T-AG-CA---TG-AG-T-
250 260 270 280 290 300 310 320
Pig CTGTGT..AAATCTACCAGCATCAAGACT...CACTGTGGGACCACTGCTTTG...TCCCATTCTCAGCTGAAATGAT.G
Hum -C--AACC-G-GGC--T--G--T-CCC-AGGG-CA-C--T-CT-CA---CCGCCCA---C--GC-GC---CTG-G-C-
330 340 350 360 370 380 390 400
Pig GAGGGCCTCATAAGAGGGGTGGACAGGGC..CTGGAGTAGAGGCCAGATCAGTGACGT..GCCTTCAGG....ACCTCCG
Hum --T----C--GTG---TT-A-T-----TT-----T-CCTC-GTTTC-GG-CT--C-AT-G-----CCTTC-G----T

Figure 2 (cont.)

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      410      420      430      440      450      460      470      480
Pig GGGAGTTAGAGCTGCCCTCTCTCAGTT.....CAGTTCCCCCCTGCTGAGAATG.TCCCTGGAAGGAAGCCAGTTAAT
Hum -----CCC-----TTG-.-C---CAACGTCGC--C-G---T---A--CTCC-G-C-TTG-CATTTC---G-T-C-G-.
      490      500      510      520      530      540      550      560
Pig AAACCTTGGTTGGATGGAATTTCCCACTCG.....
Hum --TG--GCA--TC-G--G.....CA-G-AGCAGCCGTTATTTATAGAACTGCCTGTTGGAGGTGGGGAGTCCTCCCT
      570      580      590      600      610      620      630      640
Pig .....
Hum CCATTCTTGTCCAGAAAACCTTAGCTCTCGCAGTGAGCCATGTTCTTAGTCTCCAGGGATGGATGGCCTTGTATATGG
      650      660      670      680      690      700      710      720
Pig .....
Hum ACCCCTGAGAATGAGCAATTGAGAAAACAAAACAAAAGGAACAATCCATGAACTTAGATTTTATTGGTTTCACTCAAAT

      730      740
Pig .....
Hum GCTGCAGTCATTTGACCTG
```

Figure 2 (cont.)

PigG3	MSFLEQGESRHPRAVTTSSERSHGDQGNKASRWRTRQEDVEEGPPGREGPQSRPVAESTGQEATFPKATPLAQNAFLAEVDNPPPTERDILPSCDAAS	100
HumG3	-----EN-S-----P-----S-----IR-KRRA--L-----KS-----E--QG--R--T-----L-----D--G-GT--GW-C-----T--	200
	CB91→	
PigG3	ASDSNTDHLDLGIEFSASASGDEL.GLVEEKPAPCPSPEVLLPRLGWDELQKPGAQVYMIHQEHTCYDAMATSSKLVIFDTMLEIKKAFVALVANGV	300
HumG3	-AG-S--DVE-AT--P-TE-WEC--E--L--R--L--L--QAPF-K-----R-----I--R-----V--S-QV-----T--	
HumG1	METVIS-DSSPAVENEHPQ-TPESNNS--TS--KS-R--LIP-----V--S-QV-----T--	
HumG2	AALGPAEAGM-EKLEFE-EAVEDSESG--R--RS-K--IVP-----V--T-QV-----T--	
Dros	RDSRGLPVADPPFLEKWNLS-D-EEDDS-IFVK-FRP-K--LIP-A--V--Q-LV-----Y--Y--	
Snf4	MK-TQDSQEKVSIQQLAVER..IRK-LNSK-S--VLPV-YR-IVL--S-LV--SLNV-LQ-SI	
	CB92→	
PigG3	RAAPLWDSKKQSFVGMETITDFILVHLHRYRSPVQIYEIEEHKIETWREIYLGCFKPL..VSTSPNDSLFPAVYALIKNRHRLPVLDPVSGA....V	400
HumG3	-----Q-----NI--K-A--L-----V--DS-----C--A--D-SS-R-K--I--E-N--T--	
HumG1	-----E-T--SL-----NI--K-M--L-----L--ET-----N--DA--D--S--K--I--I--N--A--	
HumG2	-----E-Q-----KI-QM--K--NASMEQL--LD--DV--HNQVM-----G-DA--YD-IKI--HS--I--AT-N--	
Dros	-----TSR-A-L--T--N-IQY-FSN-D.KFELVDKQLQDLGLKD-ERALGVDQ-DTA--H-SRP-----CLKMLES-SG-I-LI-QDEETHIREI-	
Snf4	VS-----CB93→	
PigG3	LHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETPALTALDIFVDRRVVSALPVVNETGQVGLYSRFDVIHLAAQQTYNHILDMNVG	500
HumG3	-----S-----I--KL-I-EF-K-E-MSKSLEE-Q--YANI-M-RT-T-VV--G--QH-----D-K-R--DI--K--N--EK--N--VS-T--	
HumG1	-----I--KL-I-EF-K-E-MSKSLEE-Q--YANI-M-RT-T-VV--G--QH-----D-K-R--DI--K--N--EK--N--VS-T--	
HumG2	-----I--QL-MSDM-K-A-MKQNLDE--YINI-FIHPTD--IK-N--E--I-----D-S-K--DI--K--N--EK--N--IT-T--	
Dros	-----I-R--FLYINE--K-AYMQKSLRE-K--YNNIETAD--TS-I--KK--E-----L-DSD-RL-DI-AK--N--EK--D--VSLR--	
Snf4	VSV--QY-I--VALNCRE...TH--KIP-G--N-I-QDNMKSCQM-T-VIDVIQMLTQG--SV-IID-N-YLINV-EAY--LG-IKGGI--D-SLS--	
	CB94→	
PigG3	EALRQRTLCEGLVSCQPHEITLGEVILRIVREQVHRLVLVDETHQLHLLGVVLSLSDILQALVLSPAGIDALGA*	600
HumG3	-----S-----A-----V--NDVVK-I-----TGGEKKP*	
HumG1	K--QH-SHYF--K-YL--ETI-N-L-EAE-----V--N-ADSIV-II-----I-T--AKQKETETE*	
HumG2	Q--QH-SQYF--VK-NKL-I-ETIV--AE-----V--NRKVI-II-----LY--R-S-EGV	
Dros	K-NEH-NEHF--QK-NLD-S-YTIME--AE-----V--NRKVI-II-----LY--R-S-EGV	
Snf4	---MR-SDDF--YT-TKNDK-STIM-N-RKAR--FFV--DVGR-V--LT-----KYIL-GSN*	

Figure 3

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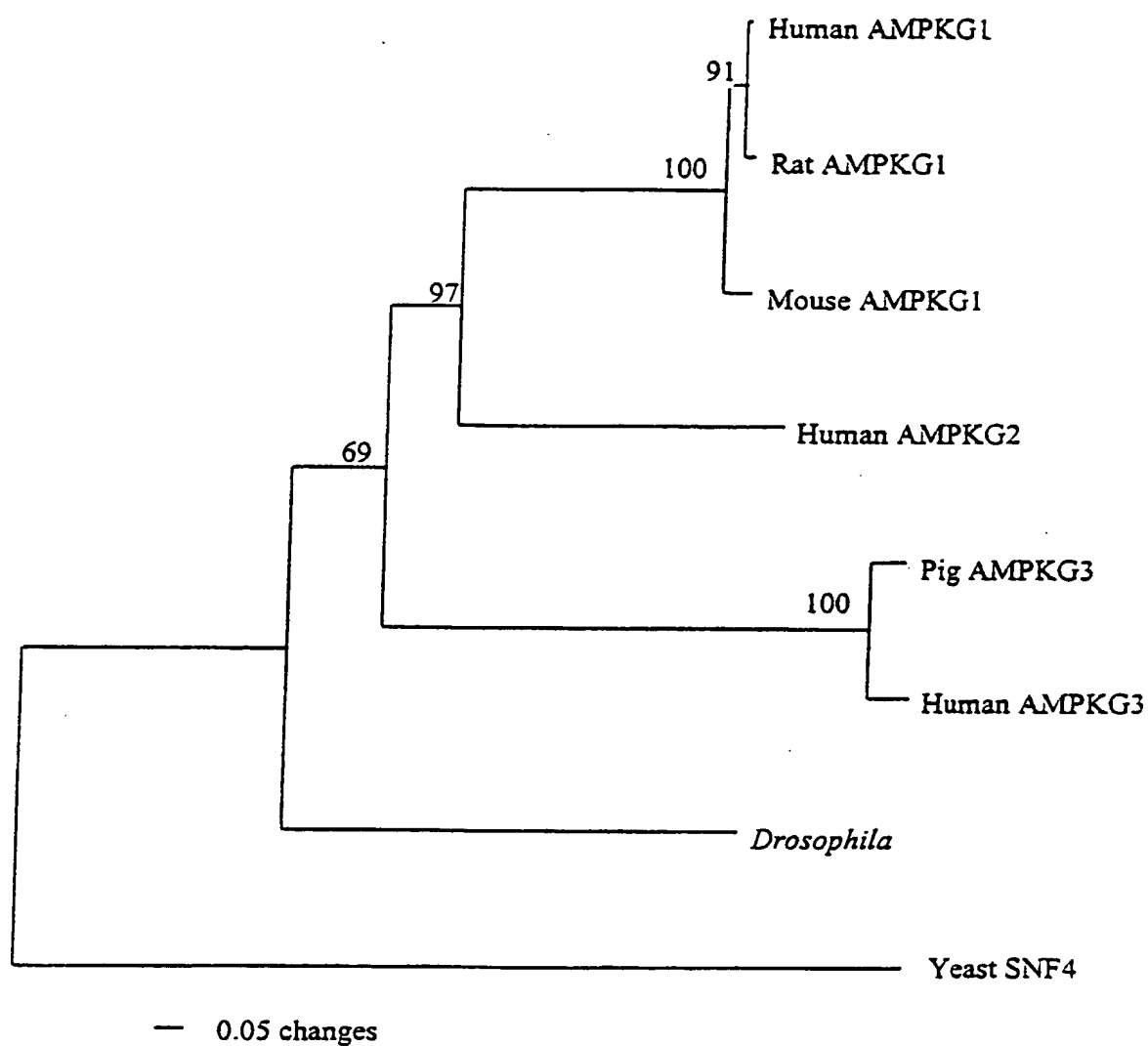


Figure 4

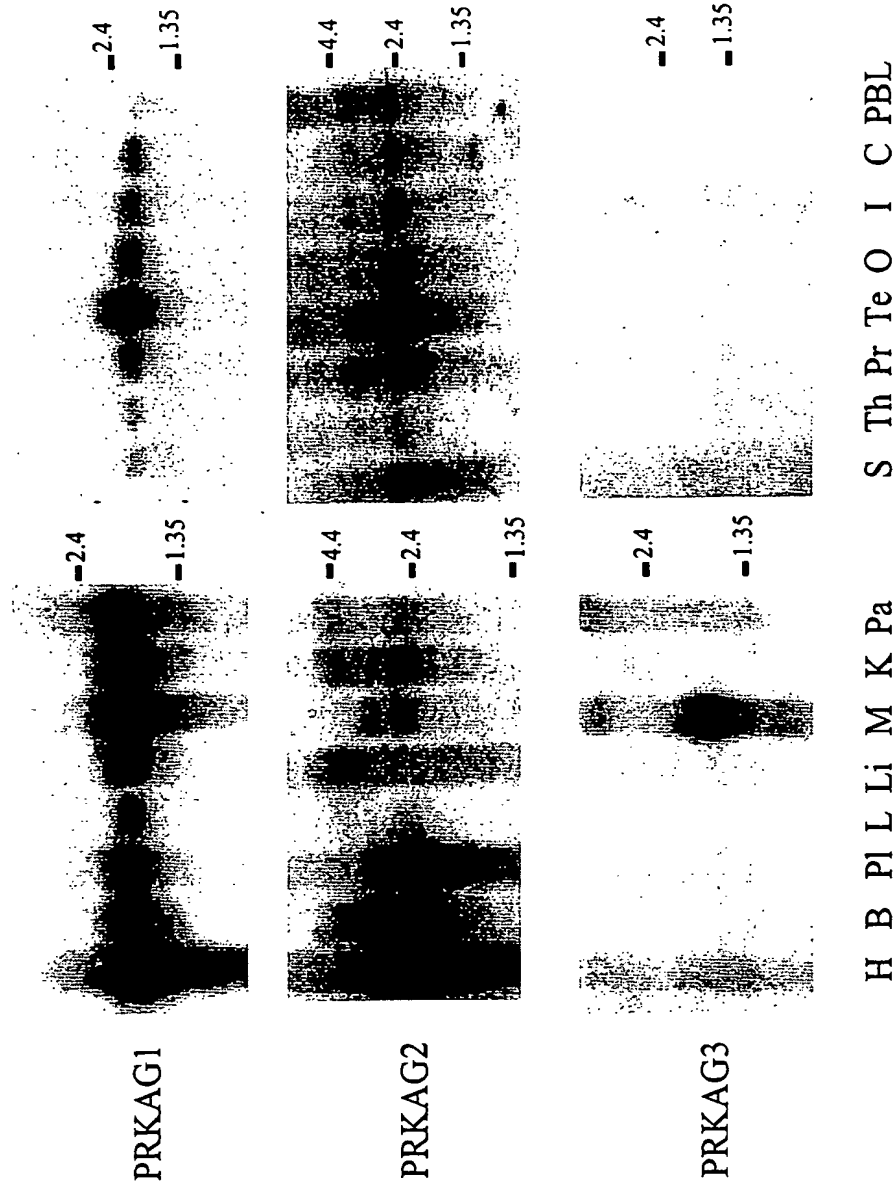


Figure 5

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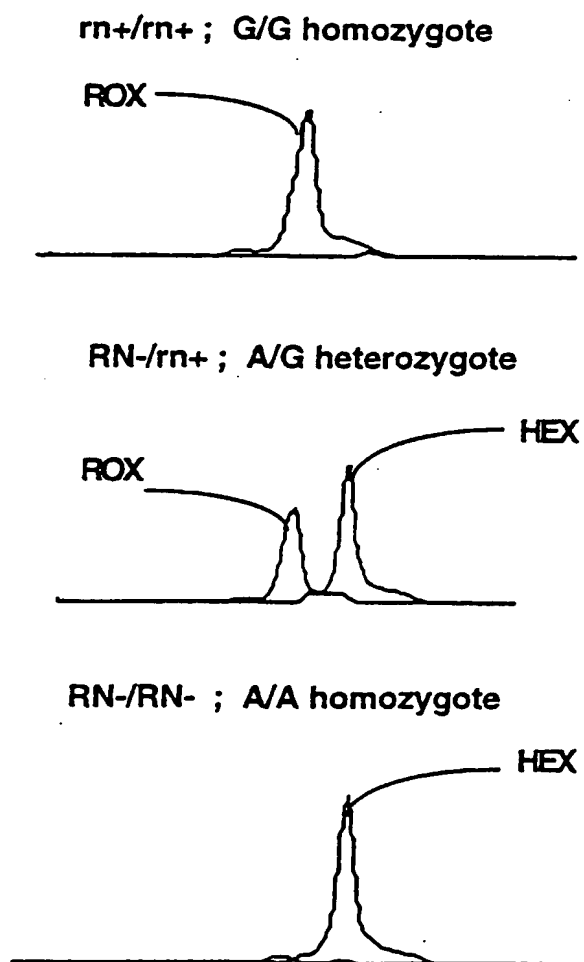


Figure 6